

(1) GENERAL INFORMATION:

- 272000

(D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Glu or Gly."

(J) PUBLICATION DATE: 20-AUG-1992

Leu Ala Lys Glu Lys Leu Gln Xaa Gln Gln Ser Asp Leu Glu Gln Glu  
1 5 10 15

Arg

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: /note= "Amino Acid 1 wherein Xaa is Ser or Arg."

(D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is  
Glu or Asp."

(D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Arg or Leu."

(D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa  
is Glu or Gly."

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln  
 1 5 10 15

Gln

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Ser or Arg."

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Glu or Asp."

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /note= "Amino Acid 9 wherein Xaa is Arg or Leu."

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 16  
 (D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa is Glu or Gly."

- (x) PUBLICATION INFORMATION:  
 (H) DOCUMENT NUMBER: WO 92/13884  
 (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa  
 1 5 10 15

Gln

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

100120-ES600660



- (ix) FEATURE:

- (ix) **FEATURE:**

- (x) PUBLICATION INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is  
Glu or Gly."

(ix) **FEATURE:**

- (A) NAME/KEY: Peptide  
(B) LOCATION: 5

- (D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is Ser or Arg."

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 10  
(D) OTHER INFORMATION: /note= "Amino Acid 10 wherein Xaa  
is Glu or Asp."

(2) SECRET

(B) LOCATION: 12

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys  
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Peptide

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "Amino Acid 3 wherein Xaa is Glu or Gly."

(A) NAME/KEY: Peptide

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is Ser or Arg."

(A) NAME/KEY: Peptide

(B) LOCATION: 11

(D) OTHER INFORMATION: /note= "Amino Acid 11 wherein Xaa  
is Glu or Asp."

(A) NAME/KEY: Peptide

(B) LOCATION: 13

(D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa  
is Arg or Leu."

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu  
 1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Amino Acid 4 wherein Xaa is Glu or Gly."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Ser or Arg."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa is Glu or Asp."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /note= "Amino Acid 14 wherein Xaa is Arg or Leu."

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys  
 1 5 10 15

Glu

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Peptide

(D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is  
Glu or Gly."

(A) NAME/KEY: Peptide

(D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Ser or Arg."

(A) NAME/KEY: Peptide

(D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa  
is Glu or Asp."

(A) NAME/KEY: Peptide

(D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa  
is Arg or Leu."

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala  
1 5 10 15

**Lys**

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is  
Glu or Gly."

(ix) FEATURE:



- (ix) **FEATURE:**

- (ix) FEATURE:

- (x) PUBLICATION INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala

(2) INFORMATION FOR SEO ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) **FEATURE:**

- (A) NAME/KEY: Peptide  
(B) LOCATION: 7  
(D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is  
Glu or Gly."

- (ix) **FEATURE:**

- (A) NAME/KEY: Peptide  
(B) LOCATION: 10  
(D) OTHER INFORMATION: /note= "Amino Acid 10 wherein Xaa  
is Ser or Arg."

- (ix) FEATURE:

- ```
(A) NAME/KEY: Peptide
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa
    is Glu or Asp."
```

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa is Arg or Leu."

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg  
 1                      5                      10                      15  
 Xaa

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Amino Acid 1 wherein Xaa is Arg or Leu."

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Glu or Gly."

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Amino Acid 11 wherein Xaa is Ser or Arg."

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa is Glu or Asp."

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Arg or Leu."

(A) NAME/KEY: Peptide

- (B) LOCATION: 9  
(D) OTHER INFORMATION: /note= "Amino Acid 9 wherein Xaa is  
Glu or Gly."

(A) NAME/KEY: Peptide

- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa  
is Ser or Arg."

(A) NAME/KEY: Peptide

- (B) LOCATION: 17  
(D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa  
is Glu or Asp."

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln  
1 5 10 15

**Xaa**

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

[illegible]

(ix) **FEATURE:**

(B) LOCATION: 1

(ix) **FEATURE:**

(B) LOCATION: 3

(ix) **FEATURE:**

(B) LOCATION: 10

(ix) FEATURE:

(B) LOCATION: 13

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Glu or Asp."

(ix) FEATURE:

- (ix) FEATURE:

- (ix) **FEATURE:**

- (x) PUBLICATION INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /note= "Amino Acid 3 wherein Xaa is  
Glu or Asp."

- (ix) **FEATURE:**

- (A) NAME/KEY: Peptide  
(B) LOCATION: 5  
(D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is  
Arg or Leu."

- (ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa  
is Glu or Gly."

(D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa  
is Ser or Arg."

(J) PUBLICATION DATE: 20-AUG-1992

## Leu

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: /note= "Amino Acid 4 wherein Xaa is  
Glu or Asp."

(D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is Arg or Leu."

(D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa is Glu or Gly."

(D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa  
is Ser or Arg."

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa  
 1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is Glu or Asp."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Arg or Leu."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /note= "Amino Acid 14 wherein Xaa is Glu or Gly."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa is Ser or Arg."

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln  
 1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His Gly
1          5          10          15
Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro Ala Ile
20          25          30
Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser
35          40          45
Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile
50          55          60
Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val Glu
65          70          75          80
Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp Gly
85          90          95
Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
100          105

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Leu Gln Glu Gln Gln Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys
1          5          10          15
Lys Asn Leu Glu Arg Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp
20          25          30
Leu Tyr Gly Arg Leu Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn
35          40          45

```



Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn  
 50 55 60  
 Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr  
 65 70 75 80  
 Asn Arg Glu Ser Ile Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His  
 85 90 95  
 Lys Gly His Leu Glu Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln  
 100 105 110  
 Lys Glu Asp Lys Ser  
 115

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His Gly Asp Ile Leu  
 1 5 10 15  
 Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro  
 20 25

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Arg Asp Leu Glu  
 1 5 10 15

Gln Arg Lys Ala Asp Thr Lys Lys  
20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Arg | Asp | Ser | Lys | Glu | Ile | Ser | Ile | Ile | Glu | Lys | Thr | Asn | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | Ile | Thr | Thr | Asn | Val | Glu | Gly | Arg | Arg | Asp | Ile | His | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | Glu | Leu | Phe | Asn | Glu | Leu | Leu | Asn | Ser | Val | Asp | Val | Asn | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Val | Lys | Glu | Asn | Ile | Leu | Glu | Glu | Ser | Gln | Val | Asn | Asp | Asp | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Asn | Ser | Leu | Val | Lys | Ser | Val | Gln | Gln | Glu | Gln | Gln | His | Asn | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Lys | Val | Glu | Glu | Ser | Val | Glu | Glu | Asn | Asp | Glu | Glu | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Asn | Val | Glu | Glu | Asn | Val | Glu | Glu | Asn | Asp | Asp | Gly | Ser | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |

FOOTNOTES

Ala Ser Ser Val Glu Glu Ser Ile Ala Ser Ser Val Asp Glu Ser Ile  
                             85                            90                            95

Asp Ser Ser Ile Glu Glu Asn Val Ala Pro Thr Val Glu Glu Ile Val  
                             100                            105                            110

Ala Pro Thr Val Glu Glu Ile Val Ala Pro Ser Val Val Glu Lys Cys  
                             115                            120                            125

Ala Pro Ser Val Glu Glu Ser Val Ala Pro Ser Val Glu Glu Ser Val  
                             130                            135                            140

Ala Glu Met Leu Lys Glu Arg  
                             145                            150

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Asp Glu Leu Phe Asn Glu Leu Leu Asn Ser Val Asp Val Asn Gly  
   1                            5                            10                            15

Glu Val Lys Glu Asn Ile Leu Glu Glu Ser Gln Val Asn Asp Asp Ile  
                             20                            25                            30

Phe Asn Ser Leu Val Lys Ser Val Gln Gln Glu Gln Gln His Asn  
                             35                            40                            45

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

2)

(2) - INFORMATION FOR SEQ ID NO:27: .....

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Ser Val Gln Gln Glu Gln Gln His Asn Val  
20 25

(2) INFORMATION FOR SEQ ID NO:28:

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Glu Ser Val Ala Glu Met Leu Lys Glu Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTGTTCTAGA TCGCTTT

17

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGAAGATA AATCT

15

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln  
1 5 10 15

Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu Lys Leu Gln Glu  
20 25 30

Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln  
35 40 45

Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu  
 50 55 60  
 Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys  
 65 70 75 80  
 Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu  
 85 90 95  
 Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys  
 100 105 110  
 Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala  
 115 120 125  
 Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg  
 130 135 140  
 Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg  
 145 150 155 160  
 Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu  
 165 170 175  
 Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln  
 180 185 190  
 Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Arg Asp Leu Glu  
 195 200 205  
 Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His  
 210 215 220  
 Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro Ala  
 225 230 235 240  
 Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln  
 245 250 255  
 Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu  
 260 265 270  
 Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val  
 275 280 285  
 Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp  
 290 295 300  
 Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAAGCGATCT AGAACAAGAG AGACGTGCTA AAGAAAAGTT GCAAGAACAA CAAAGCGATT | 60  |
| TAGAACAAGA TAGACTTGCT AAAGAAAAGT TACAAGAGCA GCAAAGCGAT TTAGAACAAG | 120 |
| AGAGACTTGC TAAAGAAAAG TTGCAAGAAC AACAAAGCGA TCTAGAACAA GAGAGACGTG | 180 |
| CTAAAGAAAA GTTGCAAGAA CAACAAAGCG ATTTAGAACA AGAGAGACGT GCTAAAGAAA | 240 |
| AGTTGCAAGA ACAACAAAGC GATTTAGAAC AAGATAGACT TGCTAAAGAA AAGTTACAAG | 300 |
| AGCAGCAAAG CGATTTAGAA CAAGAGAGAC GTGCTAAAGA AAAGTTGCAA GAACAACAAA | 360 |
| GCGATTTAGA ACAAGAGAGA CGTGCTAAAG AAAAGTTGCA AGAACAACAA AGCGATTTAG | 420 |
| AACAAGAGAG ACTTGCTAAA GAAAAGTTGC AAGAACAACA AAGCGATTTA GAACAAGAGA | 480 |
| GACGTGCTAA AGAAAAGTTG CAAGAACAAC AAAGCGATTT AGAACAAGAG AGACGTGCTA | 540 |
| AAGAAAAGTT GCAAGAACAA CAAAGCGATT TAGAACAAGA GAGACGTGCT AAAGAAAAGT | 600 |
| TGCAAGAGCA GCAAAGAGAT TTAGAACAAA GGAAGGCTGA TACGAAAAAA AATTTAGAAA | 660 |
| GAAAAAAGGA ACATGGAGAT ATATTAGCAG AGGATTTATA TGGTCGTTTA GAAATACCAG | 720 |
| CTATAGAACT TCCATCAGAA AATGAACGTG GATATTATAT ACCACATCAA TCTTCTTTAC | 780 |
| CTCAGGACAA CAGAGGGAAT AGTAGAGATT CCAAGGAAAT ATCTATAATA GAAAAACAA  | 840 |
| ATAGAGAATC TATTACAACA AATGTTGAAG GACGAAGGGA TATACATAAA CGACATCTTG | 900 |
| AAGAAAAGAA AGATGGTTCA ATAAAACCAG AACAAAAAGA AGATAAATCT            | 950 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 464 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATTCCTG ATGAACTTTT TAATGAATTA TTAAATAGTG TAGATGTTAA TGGAGAAGTA 60  
AAAGAAAATA TTTTGGAGGA AAGTCAAGTT AATGACGATA TTTTAAATAG TTTAGTAAAA 120  
AGTGTTCAAC AAGAACAACA ACACAATGTT GAAGAAAAAG TTGAAGAAAG TGTAGAAGAA 180  
AATGACGAAG AAAGTGTAGA AGAAAATGTA GAAGAAAATG TAGAAGAAAA TGACGACGGA 240  
AGTGTAGCCT CAAGTGTGTA AGAAAGTATA GCTTCAAGTG TTGATGAAAG TATAGATTCA 300  
AGTATTGAAG AAAATGTAGC TCCAAGTGT GAAGAAATCG TAGCTCCAAC TGTGTAAGAA 360  
ATTGTAGCTC CAAGTGTGTT AGAAAAGTGT GCTCCAAGTG TTGAAGAAAG TGTAGCTCCA 420  
AGTGTTGAAG AAAGTGTAGC TGAAATGTTG AAGGAAAGGA ATTC 464

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAAGTATACA TCTTCCTTCT TTAATTCTTA AAATGAAACA TATTTTGTAC ATATCATTTT 60  
ACTTTATCCT TGTTAATTTA TTGATATTTT ATATAAATGG AAAGATAATA AAGAATTCTG 120  
AAAAAGATGA AATCATAAAA TCTAACTTGA GAAGTGGTTC TTCAAATTCT AGGAATCGAA 180  
TAAATGAGGA AAATCACGAG AAGAAACACG TTTTATCTCA TAATTCATAT GAGAAAACCTA 240  
AAAATAATGA AAATAATAAA TTTTTCGATA AGGATAAAGA GTTAACGATG TCTAATGTAA 300  
AAAATGTGTC ACAAACAAAT TTCAAAGTC TTTTAAGAAA TCTTGGTGTT TCAGAGAATA 360  
TATTCCTTAA AGAAAATAAA TTAAATAAGG AAGGGAAATT AATTGAACAC ATAATAAATG 420  
ATGATGACGA TAAAAAATAA TATATTAAAG GGCAAGACGA AACAGACAA GAAGATCTTG 480  
AAGAAAAAGC AGCTAAAGAA AAGTTACAGG GGCAACAAAG CGATTCAGAA CAAGAGAGAC 540  
GTGCTAAAGA AAAGTTGCAA GAACAACAAA GCGATTTAGA ACAAGAGAGA CTTGCTAAAG 600  
AAAAGTTGCA AGAACAACAA AGCGATTTAG AACAAGAGAG ACGTGCTAAA GAAAAGTTGC 660



AAGAACAACA AAGCGATTTA GAACAAGAGA GACTTGCTAA AGAAAAGTTG CAAGAACAAC 720  
 AAAGCGATTT AGAACAAGAG AGACGTGCTA AAGAAAAGTT GCAAGAACAA CAAAGCGATT 780  
 TAGAACAAGA GAGACGTGCT AAAGAAAAGT TGCAAGAACA ACAAAGCGAT TTAGAACAAG 840  
 AGAGACTTGC TAAAGAAAAG TTACAAGAGC AGCAAAGCGA TTTAGAACAA GATAGACTTG 900  
 CTAAAGAAAA GTTGCAAGAA CAACAAAGCG ATTTAGAACA AGAGAGACGT GCTAAAGAAA 960  
 GGTGCAAGA ACAACAAAGC GATTTAGA 988

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGAAACATA TT

12

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGCGATTTA GA

12

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..954

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AAA | CAT | ATT | TTG | TAC | ATA | TCA | TTT | TAC | TTT | ATC | CTT | GTT | AAT | TTA | 48  |
| Met | Lys | His | Ile | Leu | Tyr | Ile | Ser | Phe | Tyr | Phe | Ile | Leu | Val | Asn | Leu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| TTG | ATA | TTT | CAT | ATA | AAT | GGA | AAG | ATA | ATA | AAG | AAT | TCT | GAA | AAA | GAT | 96  |
| Leu | Ile | Phe | His | Ile | Asn | Gly | Lys | Ile | Ile | Lys | Asn | Ser | Glu | Lys | Asp |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GAA | ATC | ATA | AAA | TCT | AAC | TTG | AGA | AGT | GGT | TCT | TCA | AAT | TCT | AGG | AAT | 144 |
| Glu | Ile | Ile | Lys | Ser | Asn | Leu | Arg | Ser | Gly | Ser | Ser | Asn | Ser | Arg | Asn |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| CGA | ATA | AAT | GAG | GAA | AAT | CAC | GAG | AAG | AAA | CAC | GTT | TTA | TCT | CAT | AAT | 192 |
| Arg | Ile | Asn | Glu | Glu | Asn | His | Glu | Lys | Lys | His | Val | Leu | Ser | His | Asn |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| TCA | TAT | GAG | AAA | ACT | AAA | AAT | AAT | GAA | AAT | AAT | AAA | TTT | TTC | GAT | AAG | 240 |
| Ser | Tyr | Glu | Lys | Thr | Lys | Asn | Asn | Glu | Asn | Asn | Lys | Phe | Phe | Asp | Lys |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| GAT | AAA | GAG | TTA | ACG | ATG | TCT | AAT | GTA | AAA | AAT | GTG | TCA | CAA | ACA | AAT | 288 |
| Asp | Lys | Glu | Leu | Thr | Met | Ser | Asn | Val | Lys | Asn | Val | Ser | Gln | Thr | Asn |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| TTC | AAA | AGT | CTT | TTA | AGA | AAT | CTT | GGT | GTT | TCA | GAG | AAT | ATA | TTC | CTT | 336 |
| Phe | Lys | Ser | Leu | Leu | Arg | Asn | Leu | Gly | Val | Ser | Glu | Asn | Ile | Phe | Leu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| AAA | GAA | AAT | AAA | TTA | AAT | AAG | GAA | GGG | AAA | TTA | ATT | GAA | CAC | ATA | ATA | 384 |
| Lys | Glu | Asn | Lys | Leu | Asn | Lys | Glu | Gly | Lys | Leu | Ile | Glu | His | Ile | Ile |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| AAT | GAT | GAT | GAC | GAT | AAA | AAA | AAA | TAT | ATT | AAA | GGG | CAA | GAC | GAA | AAC | 432 |
| Asn | Asp | Asp | Asp | Asp | Lys | Lys | Lys | Tyr | Ile | Lys | Gly | Gln | Asp | Glu | Asn |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| AGA | CAA | GAA | GAT | CTT | GAA | GAA | AAA | GCA | GCT | AAA | GAA | AAG | TTA | CAG | GGG | 480 |
| Arg | Gln | Glu | Asp | Leu | Glu | Glu | Lys | Ala | Ala | Lys | Glu | Lys | Leu | Gln | Gly |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| CAA | CAA | AGC | GAT | TCA | GAA | CAA | GAG | AGA | CGT | GCT | AAA | GAA | AAG | TTG | CAA | 528 |
| Gln | Gln | Ser | Asp | Ser | Glu | Gln | Glu | Arg | Arg | Ala | Lys | Glu | Lys | Leu | Gln |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CTT<br>Leu | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | 576 |
|            |            |            | 180        |            |            |            |            | 185        |            |            |            |            | 190        |            |            |     |
| CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | 624 |
|            |            | 195        |            |            |            |            | 200        |            |            |            |            | 205        |            |            |            |     |
| TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CTT<br>Leu | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | 672 |
|            |            | 210        |            |            |            | 215        |            |            |            |            | 220        |            |            |            |            |     |
| AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | 720 |
|            |            |            |            |            | 230        |            |            |            |            | 235        |            |            |            |            | 240        |     |
| GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | 768 |
|            |            |            |            | 245        |            |            |            |            | 250        |            |            |            | 255        |            |            |     |
| AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CTT<br>Leu | 816 |
|            |            |            | 260        |            |            |            |            | 265        |            |            |            |            | 270        |            |            |     |
| GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTA<br>Leu | CAA<br>Gln | GAG<br>Glu | CAG<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAT<br>Asp | AGA<br>Arg | 864 |
|            |            | 275        |            |            |            |            | 280        |            |            |            |            | 285        |            |            |            |     |
| CTT<br>Leu | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | 912 |
|            |            | 290        |            |            |            | 295        |            |            |            |            | 300        |            |            |            |            |     |
| AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AGG<br>Arg | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu |            |            | 954 |
|            | 305        |            |            |            | 310        |            |            |            |            | 315        |            |            |            |            |            |     |

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CAAGAACAAC AAAGCGATCT AGAACAAGAG AGACGTGCTA AAGAAAAGTT GCAAGAACAA 60

CAAAGCGATT TAGAACAAGA TAGACTTGCT AAAGAAAAGT TACAAGAGCA GCAAAGCGAT 120

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTAGAACAAG AGAGACTTGC TAAGAAAAGT TGCAAGAACA ACAAAGCGAT CTAGAACAAG | 180  |
| AGAGACGTGC TAAAGAAAAG TTGCAAGAAC AACAAAGCGA TTTAGAACAA GAGAGACGTG | 240  |
| CTAAAGAAAA GTTGCAAGAA CAACAAAGCG ATTTAGAACA AGATAGACTT GCTAAAGAAA | 300  |
| AGTTACAAGA GCAGCAAAGC GATTTAGAAC AAGAGAGACG TGCTAAAGAA AAGTTGCAAG | 360  |
| AACAACAAAG CGATTTAGAA CAAGAGAGAC GTGCTAAGAA AAGTTGCAAG AACAACAAAG | 420  |
| CGATTTAGAA CAAGAGAGAC TTGCTAAAGA AAAGTTGCAA GAACAACAAA GCGATTTAGA | 480  |
| ACAAGAGAGA CGTGCTAAAG AAAAGTTGCA AGAACAACAA AGCGATTTAG AACAAGAGAG | 540  |
| ACGTGCTAAG AAAAGTTGCA AGAACAACAA AGCGATTTAG AACAAGAGAG ACGTGCTAAA | 600  |
| GAAAAGTTGC AAGAGCAGCA AAGAGATTTA GAACAAAGGA AGGCTGATAC GAAAAAAAAT | 660  |
| TTAGAAAGAA AAAAGGAACA TGGAGATATA TTAGCAGAGG ATTTATATGG TCGTTTAGAA | 720  |
| ATACCAGCTA TAGAACTTCC ATCAGAAAAT GAACGTGGAT ATTATATACC ACATCAATCT | 780  |
| TGTTTACCTC AGGACAACAG AGGGAATAGT AGAGATTCCA AGGAAATATC TATAATAGAA | 840  |
| AAAACAAATA GAGAATCTAT TACAACAAAT GTTGAAGGAC GAAGGGATAT ACATAAAGGA | 900  |
| CATCTTGAAG AAAAGAAAGA TGGTTCAATA AAACCAGAAC AAAAAGAAGA TAAATCTGCT | 960  |
| GACATACAAA ATCATACATT AGAGACAGTA AATATTTCTG ATGTTAATGA TTTTCAAATA | 1020 |
| AGTAAGTATG AGGATGAAAT AAGTGCTGAA TATGACGATT CATTAATAGA TGAAGAAGAA | 1080 |
| GATGATGAAG ACTTAGACGA ATTTAAGCCT ATTGTGCAAT ATGACAATTT CCAAGATGAA | 1140 |
| GAAAACATAG GAATTTATAA AGAACTAGAA GATTTGATAG AGAAAAATGA AAATTTAGAT | 1200 |
| GATTTAGATG AAGGAATAGA AAAATCATCA GAAGAATTAT CTGAACAAAA AATAAAAAAA | 1260 |
| GGAAAGAAAT ATGAAAAAAC AAAGGATAAT AATTTTAAAC CAAATGATAA AAGTTTGTAT | 1320 |
| GATGAGCATA TTAAAAAATA TAAAAATGAT AAGCAGGTTA ATAAGGAAAA GGAAAAATTC | 1380 |
| ATAAAATCAT TGTTTCATAT ATTTGACGGA GACAATGAAA TTTTACAGAT CGTGGATGAG | 1440 |
| TTATCTGAAG ATATAACTAA ATATTTTATG AAACATAAAA AGGTTATATA TTT        | 1493 |

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGAACAAC AA

12

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGTTATATAT TT

12

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1482

## (x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: WO 92/13884

(J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG 48  
 Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys  
 1 5 10 15

TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA 96  
 Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu  
 20 25 30

AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA 144  
 Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys

| 35                                                                                                                                                    | 40 | 45 |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|-----|
| GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT<br>Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala<br>50 55 60        |    |    | 192 |
| AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT<br>Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg<br>65 70 75 80     |    |    | 240 |
| GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT AGA<br>Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg<br>85 90 95        |    |    | 288 |
| CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG<br>Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu<br>100 105 110     |    |    | 336 |
| AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA<br>Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln<br>115 120 125     |    |    | 384 |
| GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA<br>Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu<br>130 135 140     |    |    | 432 |
| CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA<br>Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu<br>145 150 155 160 |    |    | 480 |
| GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT<br>Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp<br>165 170 175     |    |    | 528 |
| TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC<br>Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser<br>180 185 190     |    |    | 576 |
| GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAG CAG CAA<br>Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln<br>195 200 205     |    |    | 624 |
| AGA GAT TTA GAA CAA AGG AAG GCT GAT ACG AAA AAA AAT TTA GAA AGA<br>Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg<br>210 215 220     |    |    | 672 |
| AAA AAG GAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA<br>Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu<br>225 230 235 240 |    |    | 720 |
| GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT TAT<br>Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr<br>245 250 255     |    |    | 768 |
| ATA CCA CAT CAA TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA<br>Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg                    |    |    | 816 |

| 260               |                   |                   |                   |                   | 265               |                   |                   |                   |                   | 270               |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GAT<br>Asp        | TCC<br>Ser        | AAG<br>Lys<br>275 | GAA<br>Glu        | ATA<br>Ile        | TCT<br>Ser        | ATA<br>Ile        | ATA<br>Ile        | GAA<br>Glu        | AAA<br>Lys        | ACA<br>Thr        | AAT<br>Asn        | AGA<br>Arg<br>285 | GAA<br>Glu        | TCT<br>Ser        | ATT<br>Ile        | 864  |
| ACA<br>Thr        | ACA<br>Thr<br>290 | AAT<br>Asn        | GTT<br>Val        | GAA<br>Glu        | GGA<br>Gly        | CGA<br>Arg<br>295 | AGG<br>Arg        | GAT<br>Asp        | ATA<br>Ile        | CAT<br>His        | AAA<br>Lys<br>300 | GGA<br>Gly        | CAT<br>His        | CTT<br>Leu        | GAA<br>Glu        | 912  |
| GAA<br>Glu<br>305 | AAG<br>Lys        | AAA<br>Lys        | GAT<br>Asp        | GGT<br>Gly        | TCA<br>Ser<br>310 | ATA<br>Ile        | AAA<br>Lys        | CCA<br>Pro        | GAA<br>Glu        | CAA<br>Gln<br>315 | AAA<br>Lys        | GAA<br>Glu        | GAT<br>Asp        | AAA<br>Lys        | TCT<br>Ser<br>320 | 960  |
| GCT<br>Ala        | GAC<br>Asp        | ATA<br>Ile        | CAA<br>Gln        | AAT<br>Asn<br>325 | CAT<br>His        | ACA<br>Thr        | TTA<br>Leu        | GAG<br>Glu        | ACA<br>Thr<br>330 | GTA<br>Val        | AAT<br>Asn        | ATT<br>Ile        | TCT<br>Ser        | GAT<br>Asp<br>335 | GTT<br>Val        | 1008 |
| AAT<br>Asn        | GAT<br>Asp        | TTT<br>Phe<br>340 | CAA<br>Gln        | ATA<br>Ile        | AGT<br>Ser        | AAG<br>Lys        | TAT<br>Tyr        | GAG<br>Glu<br>345 | GAT<br>Asp        | GAA<br>Glu        | ATA<br>Ile        | AGT<br>Ser        | GCT<br>Ala<br>350 | GAA<br>Glu        | TAT<br>Tyr        | 1056 |
| GAC<br>Asp        | GAT<br>Asp        | TCA<br>Ser<br>355 | TTA<br>Leu        | ATA<br>Ile        | GAT<br>Asp        | GAA<br>Glu        | GAA<br>Glu<br>360 | GAA<br>Glu        | GAT<br>Asp        | GAT<br>Asp        | GAA<br>Glu        | GAC<br>Asp<br>365 | TTA<br>Leu        | GAC<br>Asp        | GAA<br>Glu        | 1104 |
| TTT<br>Phe<br>370 | AAG<br>Lys        | CCT<br>Pro        | ATT<br>Ile        | GTG<br>Val        | CAA<br>Gln        | TAT<br>Tyr<br>375 | GAC<br>Asp        | AAT<br>Asn        | TTC<br>Phe        | CAA<br>Gln        | GAT<br>Asp<br>380 | GAA<br>Glu        | GAA<br>Glu        | AAC<br>Asn        | ATA<br>Ile        | 1152 |
| GGA<br>Gly<br>385 | ATT<br>Ile        | TAT<br>Tyr        | AAA<br>Lys        | GAA<br>Glu        | CTA<br>Leu<br>390 | GAA<br>Glu        | GAT<br>Asp        | TTG<br>Leu        | ATA<br>Ile        | GAG<br>Glu<br>395 | AAA<br>Lys        | AAT<br>Asn        | GAA<br>Glu        | AAT<br>Asn        | TTA<br>Leu<br>400 | 1200 |
| GAT<br>Asp        | GAT<br>Asp        | TTA<br>Leu        | GAT<br>Asp<br>405 | GAA<br>Glu        | GGA<br>Gly        | ATA<br>Ile        | GAA<br>Glu        | AAA<br>Lys        | TCA<br>Ser<br>410 | TCA<br>Ser        | GAA<br>Glu        | GAA<br>Glu        | TTA<br>Leu        | TCT<br>Ser<br>415 | GAA<br>Glu        | 1248 |
| GAA<br>Glu        | AAA<br>Lys        | ATA<br>Ile        | AAA<br>Lys<br>420 | AAA<br>Lys        | GGA<br>Gly        | AAG<br>Lys        | AAA<br>Lys        | TAT<br>Tyr<br>425 | GAA<br>Glu        | AAA<br>Lys        | ACA<br>Thr        | AAG<br>Lys        | GAT<br>Asp<br>430 | AAT<br>Asn        | AAT<br>Asn        | 1296 |
| TTT<br>Phe        | AAA<br>Lys        | CCA<br>Pro<br>435 | AAT<br>Asn        | GAT<br>Asp        | AAA<br>Lys        | AGT<br>Ser        | TTG<br>Leu<br>440 | TAT<br>Tyr        | GAT<br>Asp        | GAG<br>Glu        | CAT<br>His        | ATT<br>Ile<br>445 | AAA<br>Lys        | AAA<br>Lys        | TAT<br>Tyr        | 1344 |
| AAA<br>Lys        | AAT<br>Asn<br>450 | GAT<br>Asp        | AAG<br>Lys        | CAG<br>Gln        | GTT<br>Val        | AAT<br>Asn<br>455 | AAG<br>Lys        | GAA<br>Glu        | AAG<br>Lys        | GAA<br>Glu        | AAA<br>Lys<br>460 | TTC<br>Phe        | ATA<br>Ile        | AAA<br>Lys        | TCA<br>Ser        | 1392 |
| TTG<br>Leu<br>465 | TTT<br>Phe        | CAT<br>His        | ATA<br>Ile        | TTT<br>Phe        | GAC<br>Asp<br>470 | GGA<br>Gly        | GAC<br>Asp        | AAT<br>Asn        | GAA<br>Glu        | ATT<br>Ile        | TTA<br>Leu        | CAG<br>Gln        | ATC<br>Ile        | GTG<br>Val        | GAT<br>Asp<br>480 | 1440 |
| GAG<br>Glu        | TTA<br>Leu        | TCT<br>Ser        | GAA<br>Glu        | GAT<br>Asp        | ATA<br>Ile        | ACT<br>Thr        | AAA<br>Lys        | TAT<br>Tyr        | TTT<br>Phe        | ATG<br>Met        | AAA<br>Lys        | CTA<br>Leu        | TAA               |                   |                   | 1482 |

485

490

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..12

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAG GTT ATA TAT  
Lys Val Ile Tyr

12

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAGAACAAC AA

12

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884



(J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGAAACTAT AA

12

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1482

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG | 48  |
| Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys |     |
| 1 5 10 15                                                       |     |
| TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA | 96  |
| Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu |     |
| 20 25 30                                                        |     |
| AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA | 144 |
| Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys |     |
| 35 40 45                                                        |     |
| GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT | 192 |
| Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala |     |
| 50 55 60                                                        |     |
| AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT | 240 |
| Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg |     |
| 65 70 75 80                                                     |     |
| GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT AGA | 288 |
| Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg |     |
| 85 90 95                                                        |     |
| CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG | 336 |
| Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu |     |
| 100 105 110                                                     |     |
| AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA | 384 |
| Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| 115        |            |            |            |            | 120        |            |            |            |            | 125        |            |            |            |            |            |      |
| GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | 432  |
| 130        |            |            |            |            | 135        |            |            |            |            | 140        |            |            |            |            |            |      |
| CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CTT<br>Leu | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | TTA<br>Leu | 480  |
| 145        |            |            |            |            | 150        |            |            |            |            | 155        |            |            |            |            | 160        |      |
| GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | 528  |
| 165        |            |            |            |            | 170        |            |            |            |            | 175        |            |            |            |            |            |      |
| TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | 576  |
| 180        |            |            |            |            | 185        |            |            |            |            | 190        |            |            |            |            |            |      |
| GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | GAG<br>Glu | AGA<br>Arg | CGT<br>Arg | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | TTG<br>Leu | CAA<br>Gln | GAG<br>Glu | CAG<br>Gln | CAA<br>Gln | 624  |
| 195        |            |            |            |            | 200        |            |            |            |            | 205        |            |            |            |            |            |      |
| AGA<br>Arg | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | CAA<br>Gln | AGG<br>Arg | AAG<br>Lys | GCT<br>Ala | GAT<br>Asp | ACG<br>Thr | AAA<br>Lys | AAA<br>Lys | AAT<br>Asn | TTA<br>Leu | GAA<br>Glu | AGA<br>Arg | 672  |
| 210        |            |            |            |            | 215        |            |            |            |            | 220        |            |            |            |            |            |      |
| AAA<br>Lys | AAG<br>Lys | GAA<br>Glu | CAT<br>His | GGA<br>Gly | GAT<br>Asp | ATA<br>Ile | TTA<br>Leu | GCA<br>Ala | GAG<br>Glu | GAT<br>Asp | TTA<br>Leu | TAT<br>Tyr | GGT<br>Gly | CGT<br>Arg | TTA<br>Leu | 720  |
| 225        |            |            |            |            | 230        |            |            |            |            | 235        |            |            |            |            | 240        |      |
| GAA<br>Glu | ATA<br>Ile | CCA<br>Pro | GCT<br>Ala | ATA<br>Ile | GAA<br>Glu | CTT<br>Leu | CCA<br>Pro | TCA<br>Ser | GAA<br>Glu | AAT<br>Asn | GAA<br>Glu | CGT<br>Arg | GGA<br>Gly | TAT<br>Tyr | TAT<br>Tyr | 768  |
| 245        |            |            |            |            | 250        |            |            |            |            | 255        |            |            |            |            |            |      |
| ATA<br>Ile | CCA<br>Pro | CAT<br>His | CAA<br>Gln | TCT<br>Ser | TCT<br>Ser | TTA<br>Leu | CCT<br>Pro | CAG<br>Gln | GAC<br>Asp | AAC<br>Asn | AGA<br>Arg | GGG<br>Gly | AAT<br>Asn | AGT<br>Ser | AGA<br>Arg | 816  |
| 260        |            |            |            |            | 265        |            |            |            |            | 270        |            |            |            |            |            |      |
| GAT<br>Asp | TCC<br>Ser | AAG<br>Lys | GAA<br>Glu | ATG<br>Met | TCT<br>Ser | ATA<br>Ile | ATA<br>Ile | GAA<br>Glu | AAA<br>Lys | ACA<br>Thr | AAT<br>Asn | AGA<br>Arg | GAA<br>Glu | TCT<br>Ser | ATT<br>Ile | 864  |
| 275        |            |            |            |            | 280        |            |            |            |            | 285        |            |            |            |            |            |      |
| ACA<br>Thr | ACA<br>Thr | AAT<br>Asn | GTT<br>Val | GAA<br>Glu | GGA<br>Gly | CGA<br>Arg | AGG<br>Arg | GAT<br>Asp | ATA<br>Ile | CAT<br>His | AAA<br>Lys | GGA<br>Gly | CAT<br>His | CTT<br>Leu | GAA<br>Glu | 912  |
| 290        |            |            |            |            | 295        |            |            |            |            | 300        |            |            |            |            |            |      |
| GAA<br>Glu | AAG<br>Lys | AAA<br>Lys | GAT<br>Asp | GGT<br>Gly | TCA<br>Ser | ATA<br>Ile | AAA<br>Lys | CCA<br>Pro | GAA<br>Glu | CAA<br>Gln | AAA<br>Lys | GAA<br>Glu | GAT<br>Asp | AAA<br>Lys | TCT<br>Ser | 960  |
| 305        |            |            |            |            | 310        |            |            |            |            | 315        |            |            |            |            | 320        |      |
| GCT<br>Ala | GAC<br>Asp | ATA<br>Ile | CAA<br>Gln | AAT<br>Asn | CAT<br>His | ACA<br>Thr | TTA<br>Leu | GAG<br>Glu | ACA<br>Thr | GTA<br>Val | AAT<br>Asn | ATT<br>Ile | TCT<br>Ser | GAT<br>Asp | GTT<br>Val | 1008 |
| 325        |            |            |            |            | 330        |            |            |            |            | 335        |            |            |            |            |            |      |
| AAT<br>Asn | GAT<br>Asp | TTT<br>Phe | CAA<br>Gln | ATA<br>Ile | AGT<br>Ser | AAG<br>Lys | TAT<br>Tyr | GAG<br>Glu | GAT<br>Asp | GAA<br>Glu | ATA<br>Ile | AGT<br>Ser | GCT<br>Ala | GAA<br>Glu | TAT<br>Tyr | 1056 |

| 340 |     |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |     |  |  |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|------|
| GAC | GAT | TCA | TTA | ATA | GAT | GAA | GAA | GAA | GAT | GAT | GAA | GAC | TTA | GAC | GAA |  |  | 1104 |
| Asp | Asp | Ser | Leu | Ile | Asp | Glu | Glu | Glu | Asp | Asp | Glu | Asp | Leu | Asp | Glu |  |  |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |      |
| TTT | AAG | CCT | ATT | GTG | CAA | TAT | GAC | AAT | TTC | CAA | GAT | GAA | GAA | AAC | ATA |  |  | 1152 |
| Phe | Lys | Pro | Ile | Val | Gln | Tyr | Asp | Asn | Phe | Gln | Asp | Glu | Glu | Asn | Ile |  |  |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |      |
| GGA | ATT | TAT | AAA | GAA | CTA | GAA | GAT | TTG | ATA | GAG | AAA | AAT | GAA | AAT | TTA |  |  | 1200 |
| Gly | Ile | Tyr | Lys | Glu | Leu | Glu | Asp | Leu | Ile | Glu | Lys | Asn | Glu | Asn | Leu |  |  |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |      |
| GAT | GAT | TTA | GAT | GAA | GGA | ATA | GAA | AAA | TCA | TCA | GAA | GAA | TTA | TCT | GAA |  |  | 1248 |
| Asp | Asp | Leu | Asp | Glu | Gly | Ile | Glu | Lys | Ser | Ser | Glu | Glu | Leu | Ser | Glu |  |  |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |      |
| GAA | AAA | ATA | AAA | AAA | GGA | AAG | AAA | TAT | GAA | AAA | ACA | AAG | GAT | AAT | AAT |  |  | 1296 |
| Glu | Lys | Ile | Lys | Lys | Gly | Lys | Lys | Tyr | Glu | Lys | Thr | Lys | Asp | Asn | Asn |  |  |      |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |      |
| TTT | AAA | CCA | AAT | GAT | AAA | AGT | TTG | TAT | GAT | GAG | CAT | ATT | AAA | AAA | TAT |  |  | 1344 |
| Phe | Lys | Pro | Asn | Asp | Lys | Ser | Leu | Tyr | Asp | Glu | His | Ile | Lys | Lys | Tyr |  |  |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |      |
| AAA | AAT | GAT | AAG | CAG | GTT | AAT | AAG | GAA | AAG | GAA | AAA | TTC | ATA | AAA | TCA |  |  | 1392 |
| Lys | Asn | Asp | Lys | Gln | Val | Asn | Lys | Glu | Lys | Glu | Lys | Phe | Ile | Lys | Ser |  |  |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |      |
| TTG | TTT | CAT | ATA | TTT | GAC | GGA | GAC | AAT | GAA | ATT | TTA | CAG | ATC | GTG | GAT |  |  | 1440 |
| Leu | Phe | His | Ile | Phe | Asp | Gly | Asp | Asn | Glu | Ile | Leu | Gln | Ile | Val | Asp |  |  |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |      |
| GAG | TTA | TCT | GAA | GAT | ATA | ACT | AAA | TAT | TTT | ATG | AAA | CTA | TAA |     |     |  |  | 1482 |
| Glu | Leu | Ser | Glu | Asp | Ile | Thr | Lys | Tyr | Phe | Met | Lys | Leu |     |     |     |  |  |      |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     |     |  |  |      |

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..12

## (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAG GTT ATA TAT  
Lys Val Ile Tyr  
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